



Form 1449 (Modified)	Any Docket No: MXGNP002X1	Application No.: 09/495,668
Information Disclosure Statement By Applicant  (Use Several Sheets if Necessary)	Applicant: Selifonov et al.	
	Filing Date February 1, 2000	Group 1631

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U.S. Patent Documents

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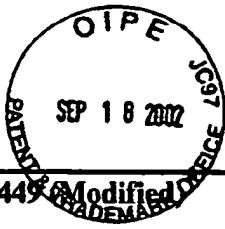
Examiner Initial	No.	Patent No.	Date	Patentee	Class	Sub-class	Filing Date
	A1	6,125,331	9/26/00	Toh			
	A2	6,403,312	6/11/02	Bassil, et al			
	A3						

Foreign Patent or Published Foreign Patent Application

Examiner Initial	No.	Document No.	Publication Date	Country or Patent Office	Class	Sub-class	Translation	
							Yes	No
	B1	WO00/47612	8/17/00	WIPO				
	B2	WO01/61344	8/23/01	WIPO				
	B3	WO00/42559	7/2/00	WIPO				
	B4	WO01/75767	10/11/01	WIPO				

Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Young et al., "Characterization of Receptor Binding Determinants of Granulocyte Colony Stimulating Factor," <i>Protein Science</i> 6:1228-1236, 1997
	C2	Dahiyat and Mayo, "Protein Design Automation," <i>Protein Science</i> , 5:895-903, (1996)
	C3	Su et al., "Coupling Backbone Flexibility and Amino Acid Sequence Selection in Protein Design," <i>Protein Science</i> , 6:1701-1707, (1997)
	C4	Voigt et al., "Computationally Focusing the Directed Evolution of Proteins," <i>Journal of Cellular Biochemistry Supplement</i> , 37:58-63 (2001)
	C5	Hellberg et al., "Minimum Analogue Peptide Sets (MAPS) for quantitative Structure-Activity Relationships," <i>Int. J. Peptide Protein Res.</i> 37:414-427 (1991)



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<input checked="" type="checkbox"/>	C6	Martin van Heel, "A New Family of Powerful Multivariate Statistical Sequence Analysis Techniques," J. Mol. Biol, 220:877-887 (1991)
<input checked="" type="checkbox"/>	C7	Goldman et al., "Estimating Protein Function From Combinatorial Sequence Data Using Decision Algorithms and Neural Networks," Drug Dev. Research 33:125-132 (1994)
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<input checked="" type="checkbox"/>	C10	Chao Zhang, "Extracting Contact Energies From Protein Structures: A Study Using a Simplified Model," Proteins: Structure, Function, and Genetics, 31:299-308 (1998)
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<input checked="" type="checkbox"/>	C12	Miyazawa et al., "An Empirical Energy Potential With a References State for Protein Fold and Sequence Recognition," Proteins: Structure, Function, and Genetics, 36:357-369 (1999)
<input checked="" type="checkbox"/>	C13	Moore et al., "Predicting Crossover Generation in DNS Shuffling," PNAS, Vol. 98, No. 6, 3226-3231 (2001)
<input checked="" type="checkbox"/>	C14	Lehman et al., "Engineering Proteins for Thermostability: the Use of Sequence Alignments Versus Rational Design and Directed Evolution," Current Opinion in Biotechnology, 13:371-375 (2001)
<input checked="" type="checkbox"/>	C15	Colleen Kelly, "A Test of the Markovian Model of DNA Evolution," Biometrics 50, 653-664, (1994)
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	C18	Jonsson, et al, "Quaintitative Sequence-Activity Modeils (QSAM)- Tool For Sequence Design", Nuclear Acid Research Vol. 21, No. 3, pp. 733-739 (1993)
	C19	Sjostrom, et al, "Signal Peptide Amino Acid Sequences In <i>Escheruchua coli</i> Contain Information Related To Final Protein Localization. A Multivariate Data Analysis", The CMBO Journal vol. 6, no. 3, pp 823-831, (1987)
	C20	Patel, et al, "Patenting Computer-Designed Peptides", Journal Of Computer-Acid Molecular Design 12 pp543-556, (1998)
	C21	Schneider, et al, "Peptide Design by Artificial Neural Networks and Computer-Based Evolutionary Search", Proc. Natl. Acad. Sci. USA, vol. 95, pp. 12179-121184, October 1998
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	C23	Bogarad, et al, "A Hierarchical Approach to Protein Molecular Evolution", Proc. Natl. Acad. Sci. USA, Vol. 96, pp. 2597-2595, March 1999
	C24	Darius, et al, "Simulated Molecular Evolution" Or Computer-Generated Artifacts?", Biophysical Journal, Vol. 67, pp. 2120-2122, November 1994
Examiner	Date Considered 2-4-05	

Examiner Initial citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.



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#### U.S. Patent Documents

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	B3							
	B4							
	B5							

#### Other Documents

Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	Martin et al., "Measuring Diversity: Experimental Design of Combinatorial Libraries for Drug Discovery," J. Med. Chem. 38, 1431-1436, 1995
	C2	Sheridan et al., "Using a Genetic Algorithm to Suggest Combinatorial Libraries," J. Chem. Inf. Compu. Sci., 35, 310-320, 1995
	C3	D.K. Agrafiotis, "Multiobjective Optimization of Combinatorial Libraries," IBM J. Res & Dev., Vol, 45, No. 3, 545-566, 2001
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O I P E  
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	A2	6,605,449 B1	08/12/03	Short	435	<del>69.1</del>	06/14/00

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Examiner Initial	No.	Author, Title, Date, Place (e.g. Journal) of Publication
	C1	SELIFONOV, Sergey A. et al., "Methods For Making Characteristics Strings, Polynucleotides And Polypeptides Having Desired Characteristics", U.S. Patent Application No. 09/416,375, Filed 10/12/1999 (Our Dkt. MXGNP001)
	C2	SELIFONOV, Sergey A. et al., "Methods For Making Character Strings, Polynucleotides And Polypeptides Having Desired Characteristics", U.S. Patent Application No. 09/494,282, Filed 1/18/2000 (Our Dkt. MXGNP001X1)
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	C5	SELIFONOV, Sergey A. et al. "Methods For Making Characteristics Strings, Polynucleotides And Polypeptides Having Desired Characteristics", PCT Application No. PCT/US00/01202, Publication No. WO 00/02560 (Our Dkt. MXGNP001X3WO)
	C6	SELIFONOV, Sergey A. et al. "In Silico Cross-Over Site Selection", PCT Application No. PCT/US01/10231, Publication No. WO 01/75767 A3 (Our Dkt. MXGNP001X4WO)
Examiner	Date Considered 2-4-05	

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